

Appl. No. : 09/539,032  
Filed : March 30, 2000

### REMARKS

Claims 1, 4-6, 8 and 9 have been amended. Thus, claims 1-9 remain presented for examination. Support for the amendments to the claims may be found in the original claims, throughout the specification (e.g., pages 5-7, 10, 14-16) and in Figure 1. Reconsideration and withdrawal of the present rejections in view of the amendments and comments presented herein are respectfully requested.

#### Rejection Under 35 U.S.C. §112, first paragraph

Claims 1-9 were rejected under 35 U.S.C. §112, first paragraph as failing to comply with the written description requirement (new matter rejection). The Examiner alleges that a step of "comparing extended conserved sequences...to host organism sequences..." as recited in step (vi) of amended claim 1, is new matter.

The recitation of step (vi) in Claim 1 finds support in steps (vii) and (viii) of claim 1 as originally filed. Step (vii) recited comparing pathogenic strain genomes against genomes of non-pathogenic strains and selecting the sequences not commonly conserved in these two groups. Step (viii) as originally filed recites validating computationally the invariant sequence motifs as potential drug target sequences by searching for the given conserved sequences in the host genome and rejecting the ones present in the host genome.

The step of comparing peptide sequences of any two organisms (A and B) is disclosed in Figure 1 of the present specification (PEPLIMP flow chart) in which the method is not limited to bacterial peptides only, and organism A or B can be bacteria or host. The presence of the specific peptides listed in the specification at page 16, Example 7, in pathogens, and their absence in host organisms, can be validated using the steps of the present invention, specifically comparison of pathogen and host genomes. This comparison step is an inherent component of the present invention.

The Examiner states that the "original claim steps are clearly directed to comparison of nucleic acid sequences (i.e. genomic material)." (Office Action at page 3). Rather, the invention is clearly directed to comparison of the genomes at the peptide level.

Appl. No. : 09/539,032  
Filed : March 30, 2000

Thus, claim 1 as amended does not include new matter. In view of the comments provided above, Applicants respectfully request reconsideration and withdrawal of the rejection under 35 U.S.C. §112, first paragraph.

**Rejection Under 35 U.S.C. §112, second paragraph**

Claims 1-9 were rejected under 35 U.S.C. §112, second paragraph, as being indefinite. The Examiner alleges that the recitation of "the conserved peptide motifs" in lines 1-2 of claim 4, and "the...conserved peptide sequences" in line 2 of claims 5 and 6, have insufficient antecedent basis in claim 1. Claims 4-6 as amended recite "extended conserved peptide sequences" which finds proper antecedent basis in step v) of claim 1.

With regard to claim 5, the Examiner states that the recitation of increasing the number of conserved peptide sequences "by increasing the relatedness" among organisms is unclear. The specification at page 14 (example 2) shows that the number of conserved peptide sequences is increased by the relatedness of the organisms being compared. For example, the number of invariant peptides among pathogenic + non-pathogenic, pathogenic and non-pathogenic organisms is 164, 206, and 601, respectively, demonstrating an increased number of conserved peptide sequences by increasing the relatedness among organisms. Thus, a group of pathogenic + non-pathogenic organisms contains fewer invariant peptides compared to either pathogenic or non-pathogenic organisms which each comprise closely related members. Thus, claim 5 is fully definite as written.

The Examiner contends that the recitation of "transporter" in claim 6 is indefinite since there are over 200,000 "transporter" proteins in the NCBI database with no structural or sequence relationship. Claim 6 as amended no longer recites this term.

Claim 8 was rejected based on the recitation of "the organism" in the last line of claim 1. Claim 8 as amended recites "the selected organism" which finds support in steps i) and iii) of claim 1.

The Examiner alleges that the recitation of iteratively comparing "data" on matched peptide locations in claim 9 is indefinite since claim 1 does not recite "peptide locations" or "data." Claim 9 as amended recites "peptide sequences" which finds support in claim 1, and claim 1 has been amended to recite "to provide locations of said matched common peptide

Appl. No. : 09/539,032  
Filed : March 30, 2000

sequences" which is clearly a result of computationally locating the matched common peptide sequences in the protein sequences of step i) as recited in step IV) of claim 1.

In view of the amendments and comments presented above, Applicants respectfully request reconsideration and withdrawal of the rejections under 35 U.S.C. §112, second paragraph.

### CONCLUSION

Applicants have made an earnest effort to respond to all objections and rejections set forth in the Office Action, and submit that all claims are in condition for allowance. If any issues remain that could be resolved by telephone, the Examiner is cordially invited to contact the undersigned at the telephone number provided below. Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

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